

FIG. 1

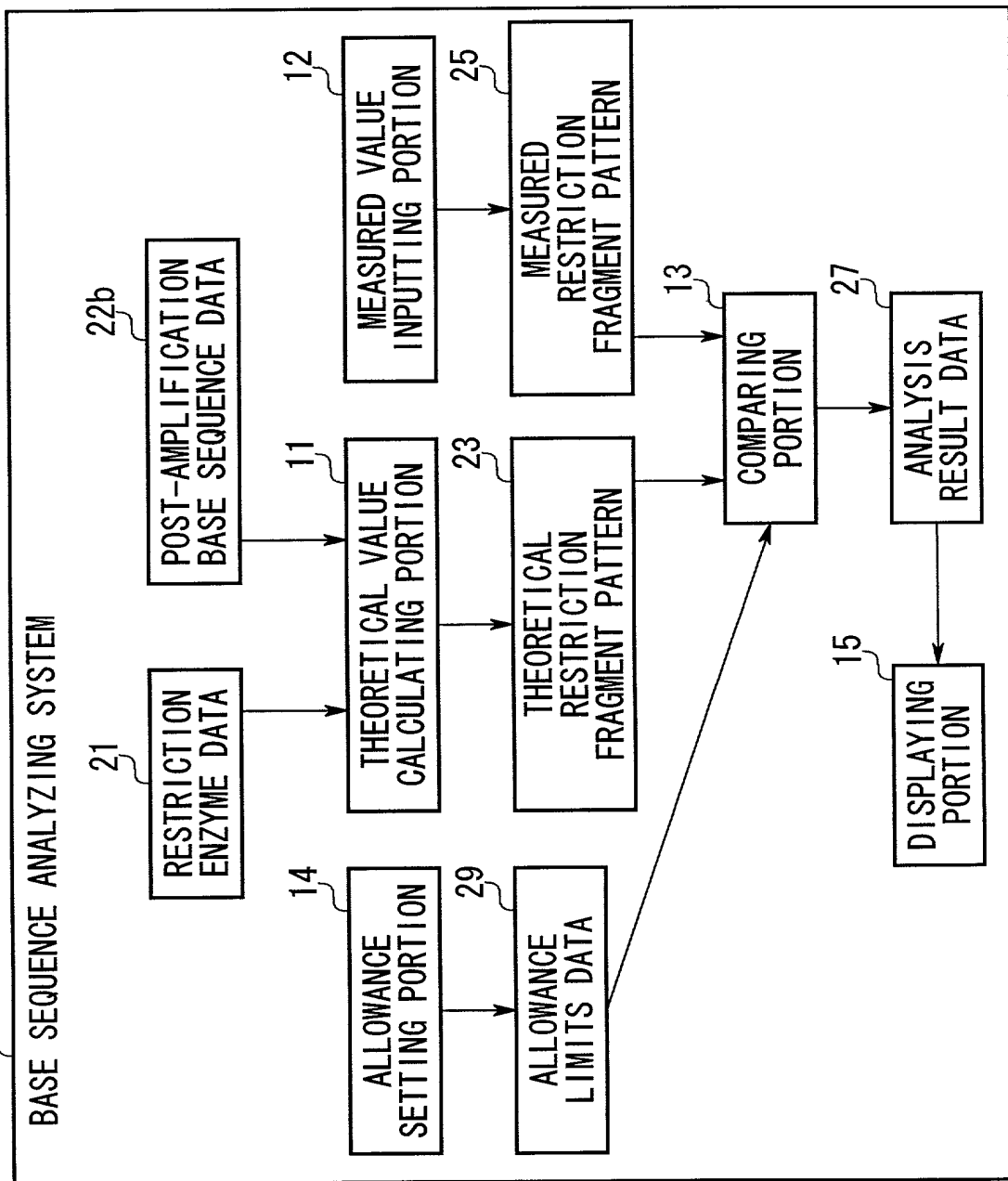


FIG. 2

LOCUS RSP16SRRZ 1490 bp rRNA BCT 04-DEC-1995
DEFINITION Rhodospirillum salexigens 16S ribosomal RNA.
ACCESSION M59070
NID g175871
VERSION M59070.1 GI:175871
KEYWORDS 16S ribosomal RNA.
SOURCE Rhodospirillum salexigens rRNA.
ORGANISM Rhodothalassium salexigens
Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
Rhodothalassium.
REFERENCE 1 (bases 1 to 1490)
AUTHORS Woese, C. R.
TITLE A phylogenetic analysis of the some purple bacteria
JOURNAL Unpublished (1991)
FEATURES Location/Qualifiers
source 1..1490
/organism="Rhodothalassium salexigens"
/db_xref="taxon:1086"
/tissue_lib="DSM 2132"
rRNA 1..1490
/gene="16S rRNA"
/product="16S ribosomal RNA"
gene 1..1490
/gene="16S rRNA"
BASE COUNT 342 a 343 c 472 g 284 t 49 others

09900875-071001

FIG. 3

ORIGIN

1 gctcagaacg aacgctggcg gcaggcctaa cacatgcaag tcgagcgcan nccttcgggg
61 gtnagcggcg gacgggtgag taacgcgtgg gaacctgctc agggctctgg gataactgct
121 ggaaacggca gctaataccg gatacgccgt attgggaaag aaattcggcc ttggatgggc
181 ccgcgtttgga ttagctagat ggtggggtaa cggcctacca tggcgacgat ccatagctgg
241 tttagagagga tgatcagcca cactgggact gagacacggc ccagactcct acgggaggca
301 gcagtgggga atcttagaca atgggggcaa ccctgatcta gccatgccgc gtgagtgatg
361 aaggccttag ggttgtaaag ctctttcagc agggaagata atgactgtac ctgcagaaga
421 agctccggct aactccgtgc cagcagccgc ggtaatacgg agngggcnag cgttgttcgg
481 aattactggg cgtaaagcgc gcgtaggcgg atcggtcagt tgggggtgaa agcccggggc
541 tcaacctcgg aactgccctc aaaactaccg atcnagagtt cgggagaggt aagcgggaatt
601 ccagtgtag aggtgaaatt cgtagatatt gggaagaaca ccagtggcga aggcggctta
661 ctggaccgat actgacgctg aggtgcnaaa gcgtggggag caaacaggat tagataccct
721 ggtagtccac gccgtaaacg atgggtgcta gatgtcgggg ctcttagagt ttcggtatcg
781 cagctaacgc attaagcacc ccgccngggg agtacggccg caaggttaaa actcaaagga
841 attgacgggg gcnngcacaa gcggtggagc atgtggttta attcgaanna acgcgcagaa
901 ccttaccagc tcttgacatc ccgggacgac ttccagagat ggattttttc acttcggtga
961 cccgngaca ggtgctgcat ggctgtcgtc agctcgtgtc gtgagatgt

//

09000376-01001

FIG. 4

RESTRICTION ENZYME DATA

RESTRICTION ENZYME NUMBER	RESTRICTION ENZYME NAME	RECOGNITION SITE	RESTRICTION SITE
1	AluI	agct	2
2	HaeIII	ggcc	2
3	RsaI	gtac	2
4	ScrFI	ccngg	2
5	HhaI	gcgc	2
6	BamHI	ggatcc	1
7	EcoRI	gaatt	1
8	HindIII	aagctt	1
9	PstI	ctgcag	5
10	PvuII	cagctg	3
11	SalI	gagctc	5
12	SmaI	cccggg	3
13	XbaI	tctaga	1

FIG. 5

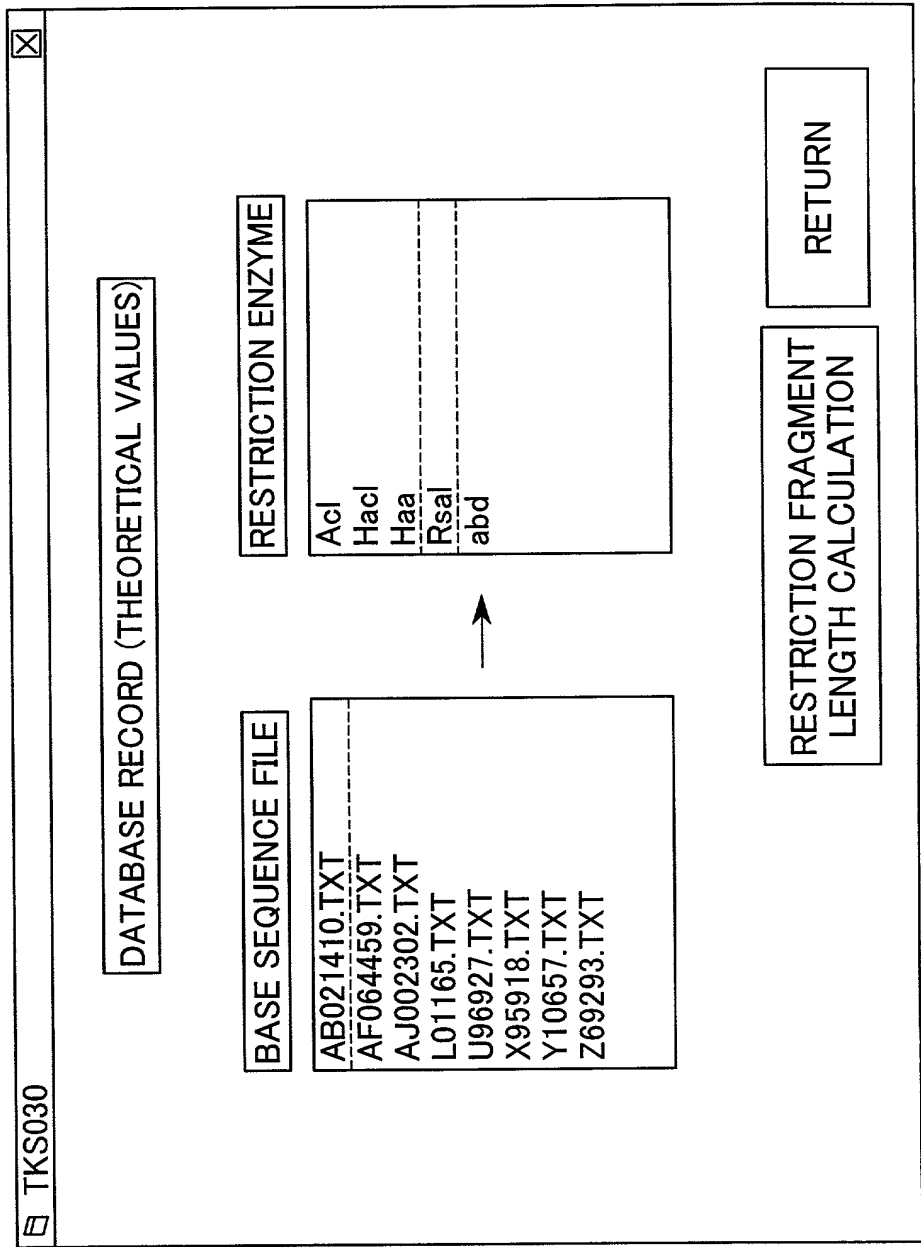


FIG. 6

THEORETICAL RESTRICTION FRAGMENT PATTERNS

DNA NUMBER	NUMERICAL VALUE SECTION	GROUP NAME	NAME OF ORGANISM	NAME OF GENE	RESTRICTION ENZYME NUMBER	RESTRICTION FRAGMENT LENGTH VALUE
AB000278	1		Vibrio ilio piscarius	16S rRNA; 16S ribosomal RNA	2	204
AB000278	1		Vibrio ilio piscarius	16S rRNA; 16S ribosomal RNA	5	509
AB000278	1		Vibrio ilio piscarius	16S rRNA; 16S ribosomal RNA	5	542
AB000278	1		Vibrio ilio piscarius	16S rRNA; 16S ribosomal RNA	3	194
AB000278	1		Vibrio ilio piscarius	16S rRNA; 16S ribosomal RNA	3	457
AB000278	1		Vibrio ilio piscarius	16S rRNA; 16S ribosomal RNA	3	400
AB000278	1		Vibrio ilio piscarius	16S rRNA; 16S ribosomal RNA	2	156
AB000278	1		Vibrio ilio piscarius	16S rRNA; 16S ribosomal RNA	2	90
AB000278	1		Vibrio ilio piscarius	16S rRNA; 16S ribosomal RNA	2	317
AB000278	1		Vibrio ilio piscarius	16S rRNA; 16S ribosomal RNA	2	169
AB000278	1		Vibrio ilio piscarius	16S rRNA; 16S ribosomal RNA	1	550
AB000278	1		Vibrio ilio piscarius	16S rRNA; 16S ribosomal RNA	1	180
AB000278	1		Vibrio ilio piscarius	16S rRNA; 16S ribosomal RNA	1	79
AB000278	1		Vibrio ilio piscarius	16S rRNA; 16S ribosomal RNA	1	87
AB000278	1		Vibrio ilio piscarius	16S rRNA; 16S ribosomal RNA	2	105
AB038030	1		Vibrio splendidus	16S ribosomal RNA	2	156
AB038030	1		Vibrio splendidus	16S ribosomal RNA	5	509
AB038030	1		Vibrio splendidus	16S ribosomal RNA	5	565
AB038030	1		Vibrio splendidus	16S ribosomal RNA	4	1074
AB038030	1		Vibrio splendidus	16S ribosomal RNA	3	194
AB038030	1		Vibrio splendidus	16S ribosomal RNA	3	234
AB038030	1		Vibrio splendidus	16S ribosomal RNA	3	223
AB038030	1		Vibrio splendidus	16S ribosomal RNA	3	423
AB038030	1		Vibrio splendidus	16S ribosomal RNA	2	90
AB038030	1		Vibrio splendidus	16S ribosomal RNA	1	175
AB038030	1		Vibrio splendidus	16S ribosomal RNA	2	204
AB038030	1		Vibrio splendidus	16S ribosomal RNA	2	317
AB038030	1		Vibrio splendidus	16S ribosomal RNA	2	105
AB038030	1		Vibrio splendidus	16S ribosomal RNA	1	236
AB038030	1		Vibrio splendidus	16S ribosomal RNA	1	572

FIG. 7

TKS040

DATABASE RECORDING (MEASURED VALUE)

MOLECULAR WEIGHT FILE

Deni01(Ha).txt
DNA.xls

GROUP NAME

AP

DNA NUMBER

AP1

RESTRICTION ENZYME

AluI

RESTRICTION FRAGMENT LENGTH

100	200	300					

ENTER

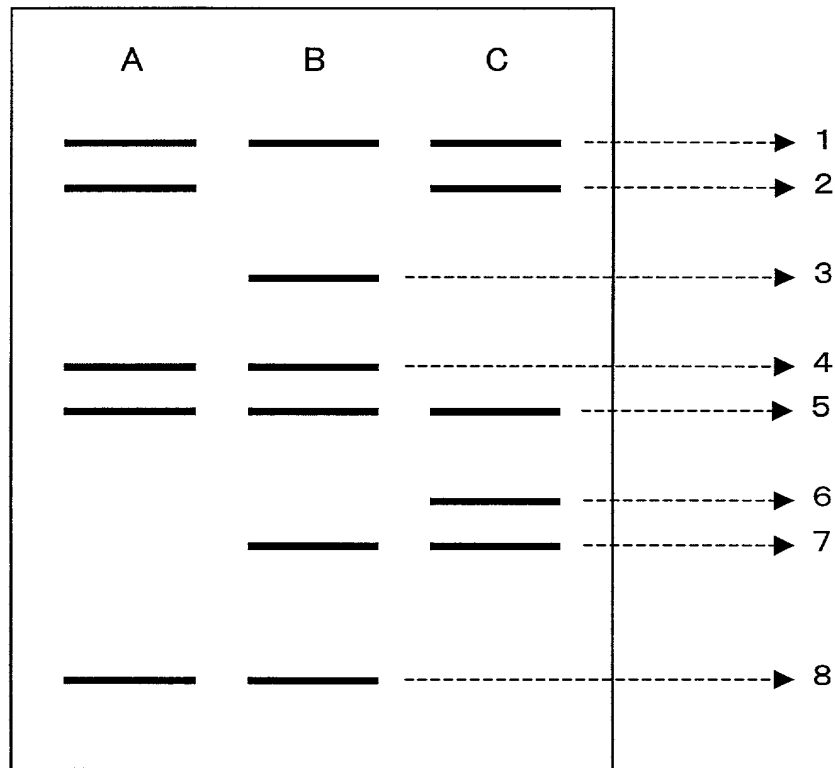
RETURN

FIG. 8

MEASURED RESTRICTION FRAGMENT PATTERNS

DNA NUMBER	NUMERICAL VALUE SECTION	GROUP NAME	NAME OF ORGANISM	NAME OF GENE	RESTRICTION ENZYME NUMBER	MEASURED RESTRICTION FRAGMENT LENGTH VALUE
AP1	2	AP			1	100
AP1	2	AP			1	200
AP1	2	AP			1	300

FIG. 9



	A	B	C	D
A	—	—	—	—
B	0.7	—	—	—
C	0.8	0.5	—	—
D	0.1	0.4	0.3	—

FIG. 10A

	A+C	B	D
A+C	—	—	—
B	0.6 (*1)	—	—
D	0.2 (*2)	0.4	—

*1

$$S(B, A + C) = \frac{S(B, A) + S(B, C)}{2}$$

*2

$$S(D, A + C) = \frac{S(D, A) + S(D, C)}{2}$$

FIG. 10B

	(A+C)+B	D
(A+C)+B	—	—
D	0.3 (*3)	—

*3

$$S(D, (A + C) + B) = \frac{S(D, A + C) + S(D, B)}{2}$$

FIG. 10C

FIG. 11

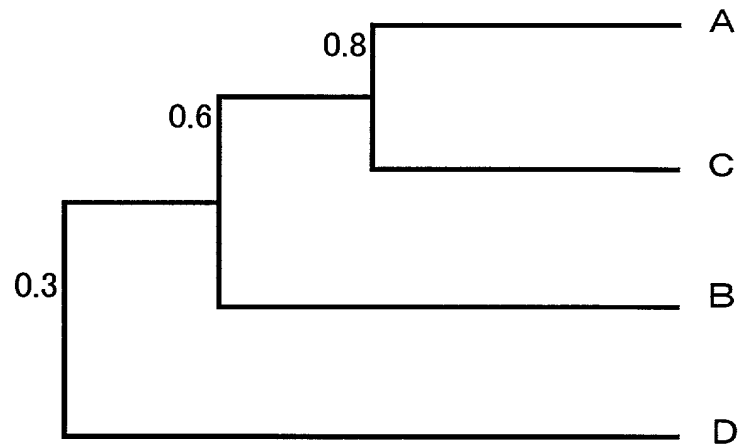


FIG. 12

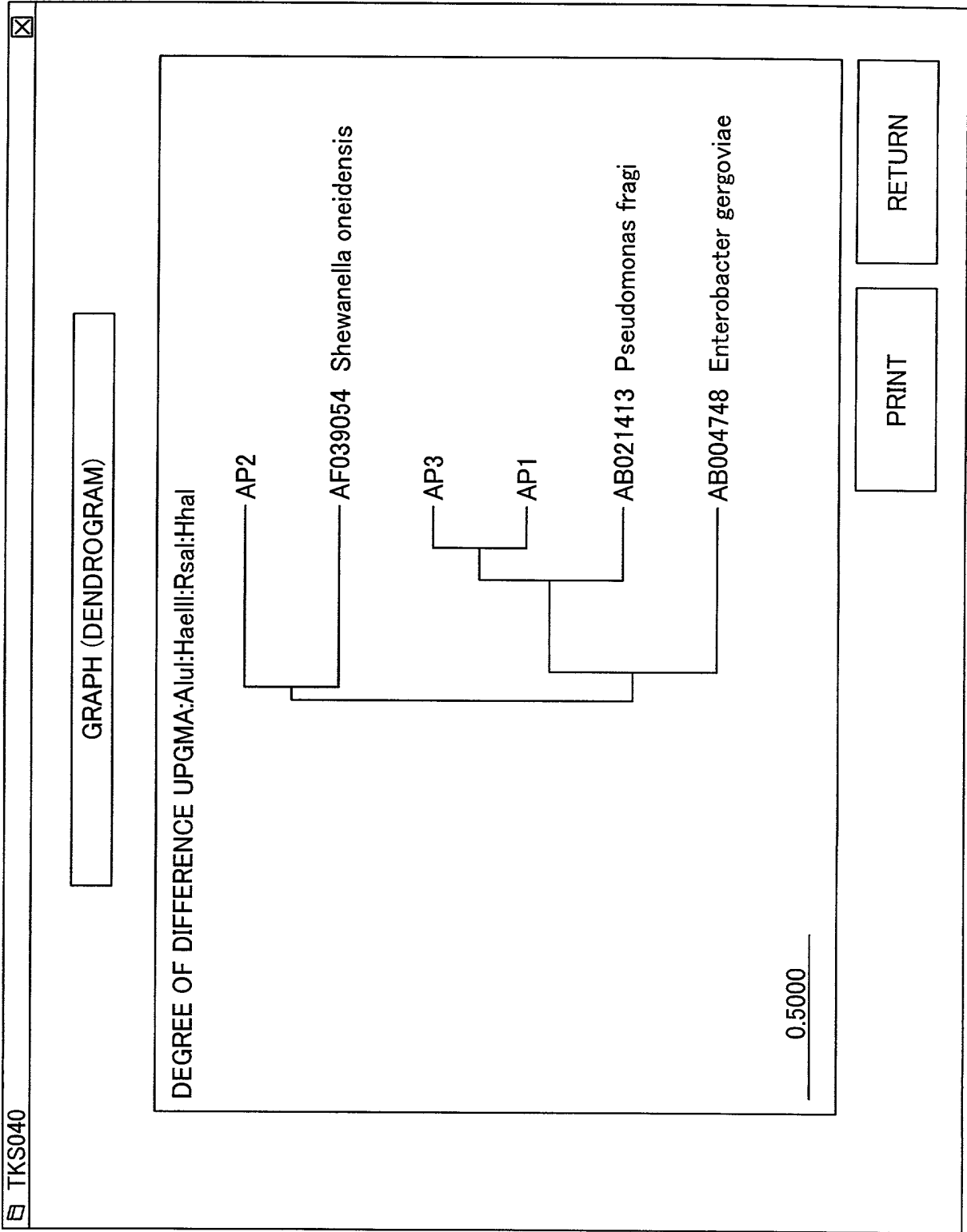
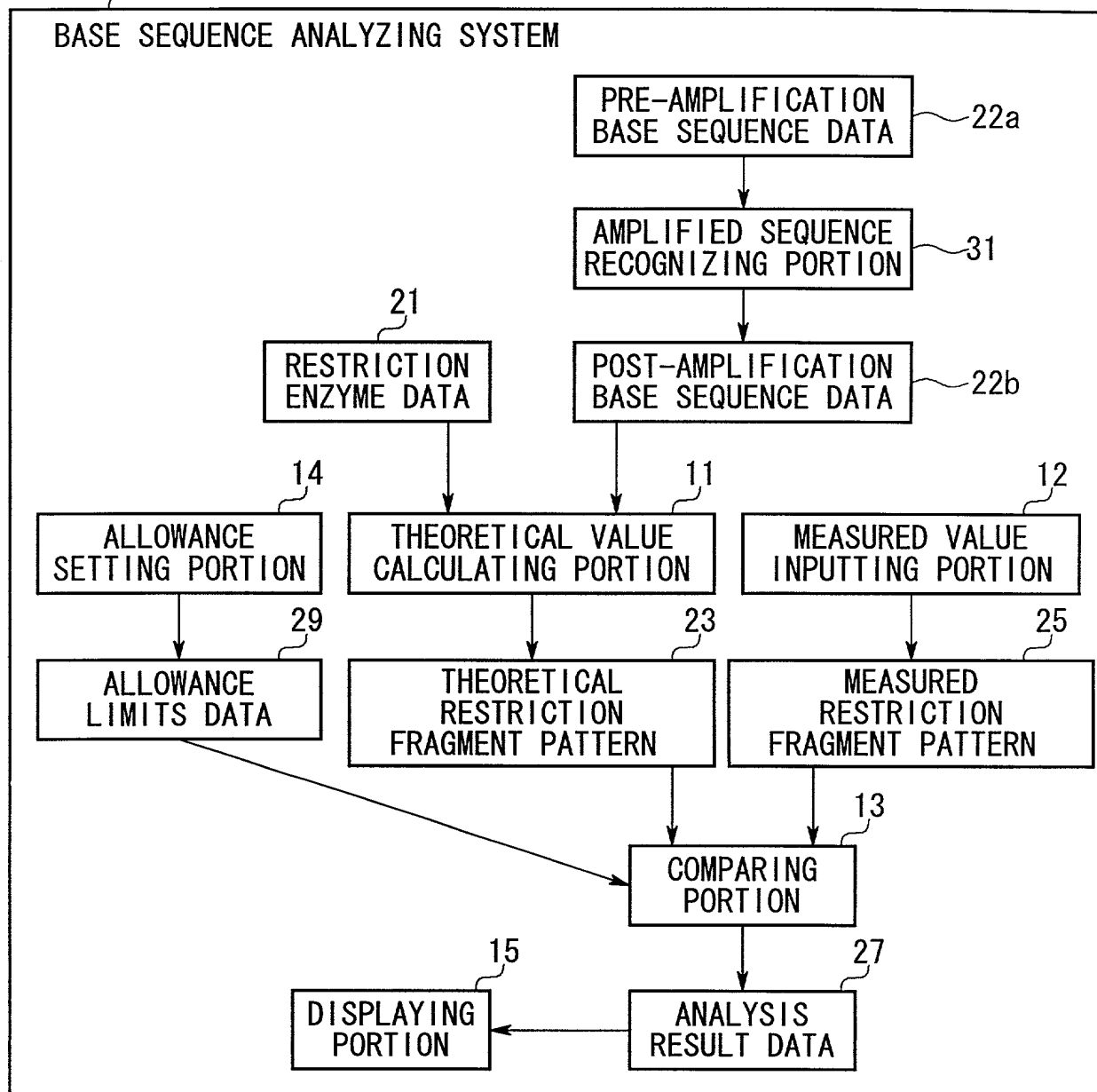


FIG. 13



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FIG. 14

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/tissue_lib="DSM 2132"
rRNA 1..1490
/gene="16S rRNA"
/product="16S ribosomal RNA"
gene 1..1490
/gene="16S rRNA"
BASE COUNT 342 a 343 c 472 g 284 t 49 others

09900876-071001

FIG. 15

ORIGIN

1 ncaacatgag agttt gatcc tggctcagaa cgaacgctgg cggcaggcct aacacatgca
61 agtcgagcgc anncccttcgg gggtnagcgg cggacgggtg agtaacgcgt gggaacctgc
121 tcagggctct gggataactg ctggaaacgg cagctaatac cggatacgcc gtattgggaa
181 agaaattcgg ccttggatgg gccgcggttg gattagctag atggtgggggt aacggcctac
241 catggcgacg atccatagct ggtttgagag gatgatcagc cacactggga ctgagacacg
301 gccagactc ctacgggagg cagcagtggg gaactctaga caatgggggc aacctgac
361 tagccatgcc gcgtgagtga tgaaggcctt agggttgtaa agctctttca gcagggaaga
421 taatgactgt acctgcagaa gaagctccgg ctaactccgt gccagcagcc gcggtaatac
481 ggagngggcn agcgttgttc ggaattactg ggcgtaaagc gcgcgtaggc ggatcgggtc
541 gttgggggtg aaagcccggg gctcaacctc ggaactgccc tcaaaaactac cgatcnagag
601 ttcgggagag gtaagcggaa ttcccagtgt agaggigaaa ttcgtagata ttgggaagaa
661 caccagtggc gaaggcggct tactggaccg atactgacgc tgagggtgna aagcgtgggg
721 agcaaacagg attagatacc ctggtagtcc acgccgtaaa cgatgggtgc tagatgtcgg
781 ggctcttaga gtttcgggtat cgcagctaac gcattaagca ccccgccngg ggagtacggc
841 cgcaaggtta aaactcaaag gaattgacgg gggcnngcac aagcgggtga gcatgtggtt
901 taattcgaan naacgcgcag aaccttacca gctcttgaca tcccgggacg acttccagag
961 atggattttt tcacttcggt gacccgnga cagggtgtgc atggctgtcg tcagctcgtg
1021 tcgtgagatg ttgggttaag tccncaacg agcgcaacc cgcaccttag ttgccagcat
1081 ttggttgggg actctaaggg aactgccggt gataagccgg aggaagggtg ggatgacgtc
1141 aagtctcat ggcccttatg ggctgggcta cacacgtgct acaatggcgg tgacagaggg
1201 cagcgagcct gcgagggtga gcgaatctct aaaagccgtc tcagttcgga ttgttctctg
1261 caactcgaga gcatgaagg ggaatcgcta gtaatcgcg atcagcatgc cgcggtgaat
1321 acgttcccgg gnnttgatca caccgccgt cacacatgg gagttgggtt gaccogaaga
1381 cggtagacta acccgaaagg ggggcagncg gccacggtca ggtagcgac tggggtnnnn
1441 nngtaacaag nnnnnnnnnn nnnnnnnnnn nnnngatca cctcctttct

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FIG. 16

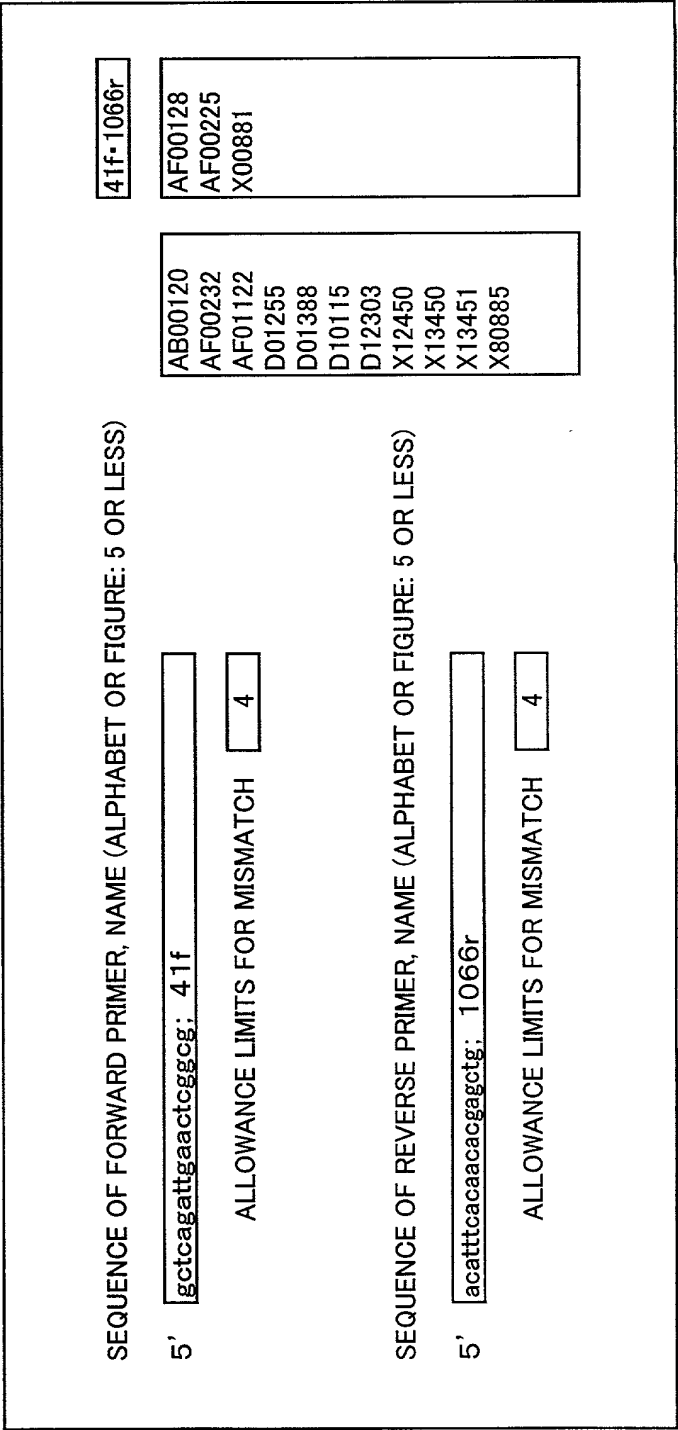
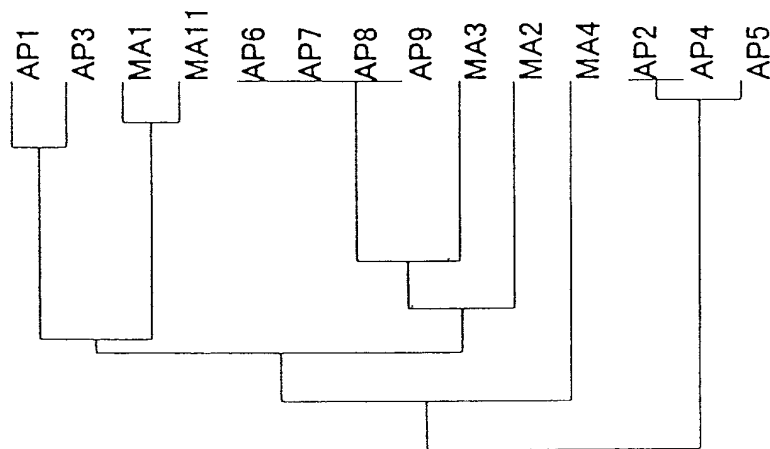


FIG. 17

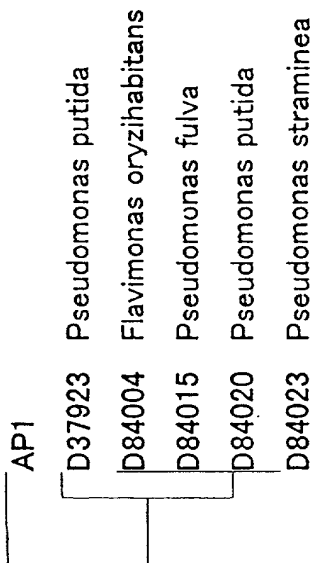
DEGREE OF DIFFERENCE UPGMA:Alul:HaeIII:RsaI:HhaI



0.5000

FIG. 18

DEGREE OF DIFFERENCE UPGMA:Alul:HaeIII:RsaI:HhaI



0.5000

FIG. 19

DEGREE OF DIFFERENCE UPGMA:AluI:HaeIII:RsaI:HhaI

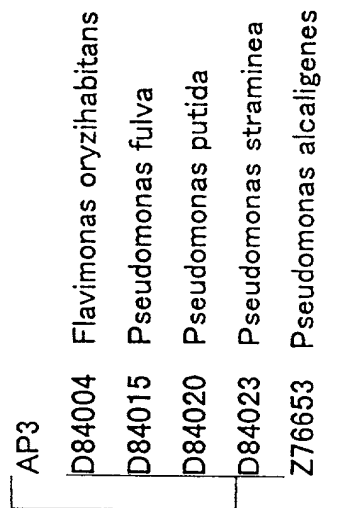
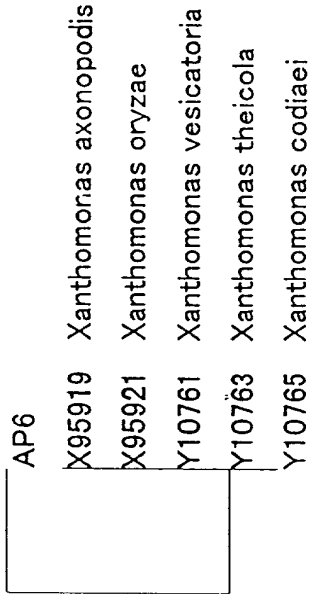


FIG. 20

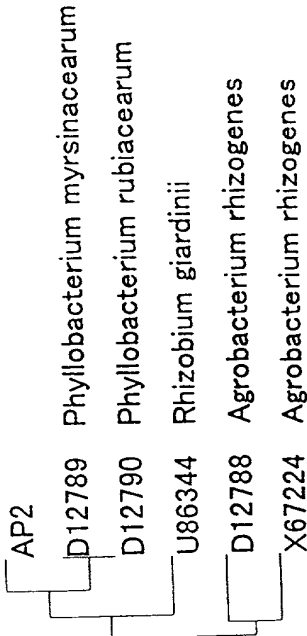
DEGREE OF DIFFERENCE UPGMA:Alul:HaeIII:RsaI:HhaI



0.5000

FIG. 21

DEGREE OF DIFFERENCE UPGMA:AluI:HaeIII:RsaI:HhaI



0.5000

FIG. 22

DEGREE OF DIFFERENCE UPGMA:AluI:HaeIII:RsaI:HhaI

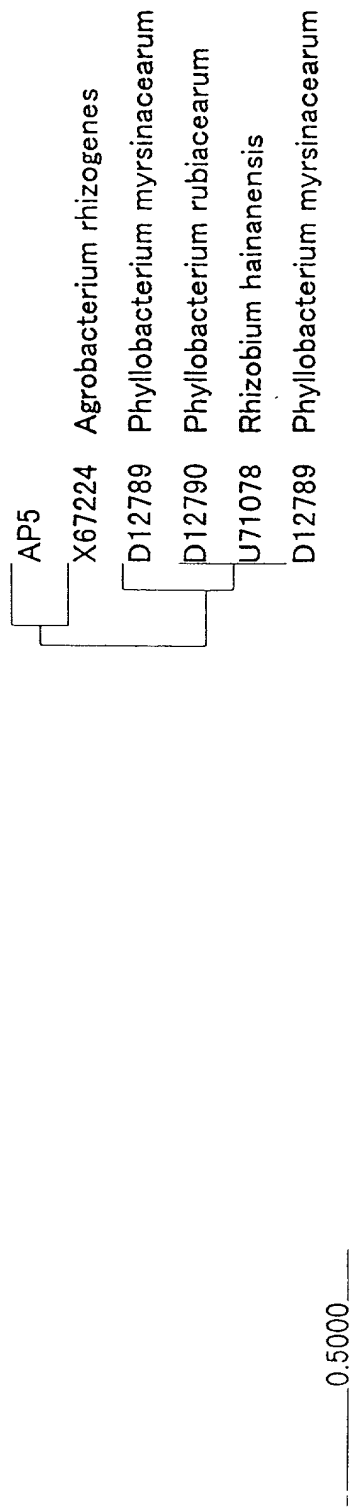
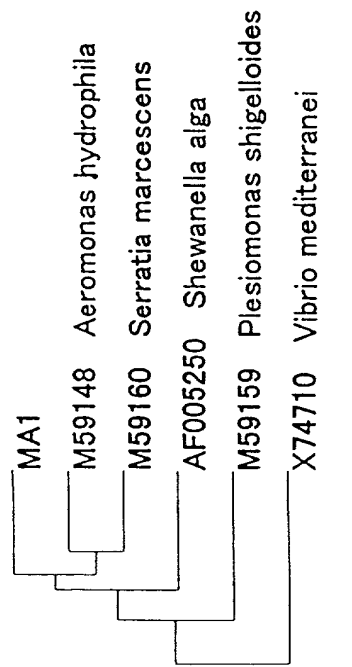


FIG. 23

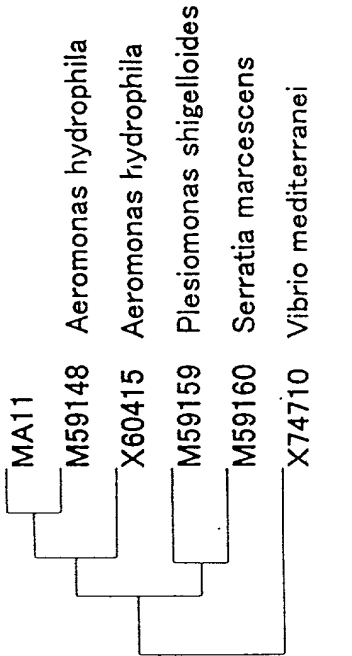
DEGREE OF DIFFERENCE UPGMA:Alut:HaeIII:RsaI:HhaI



0.5000

FIG. 24

DEGREE OF DIFFERENCE UPGMA:Alul:HaeIII:RsaI:HhaI



0.5000

FIG. 25

DEGREE OF DIFFERENCE UPGMA:Alul:HaeIII:RsaI:HhaI

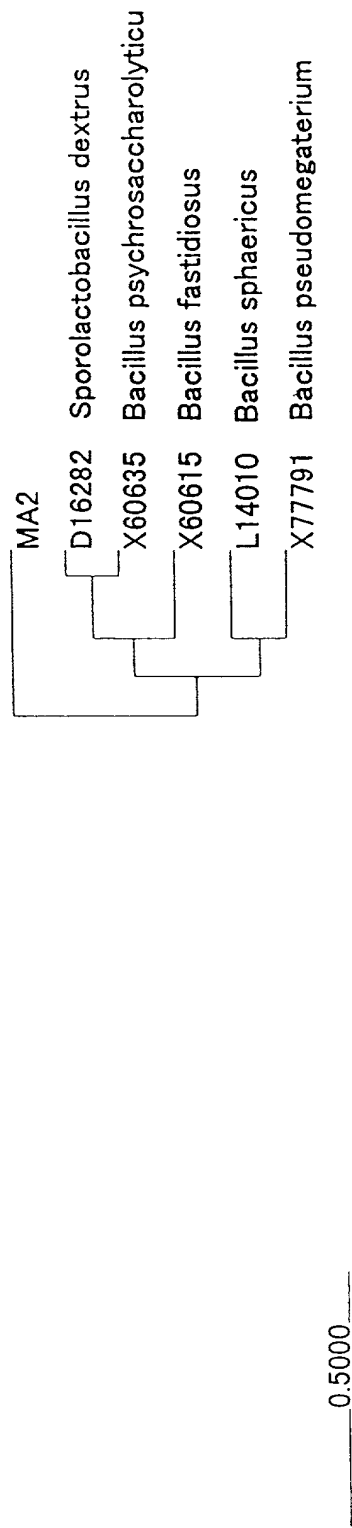
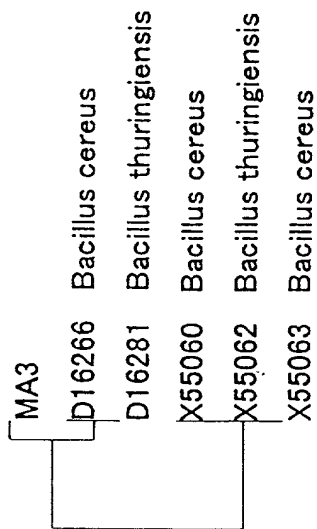


FIG. 26

DEGREE OF DIFFERENCE UPGMA:Alul:HaeIII:RsaI:HhaI



0.5000

FIG. 27

DEGREE OF DIFFERENCE UPGMA:Alul:HaeIII:RsaI:HhaI

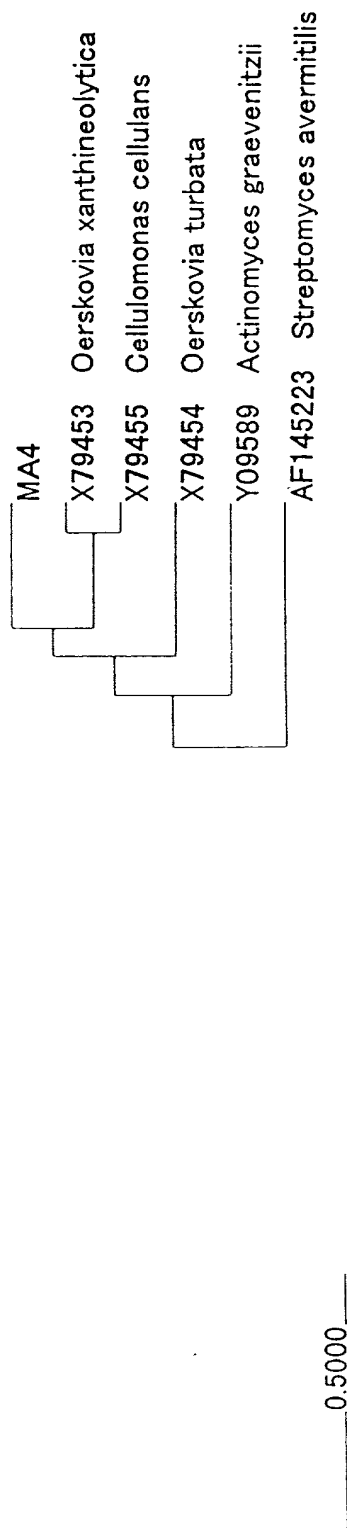
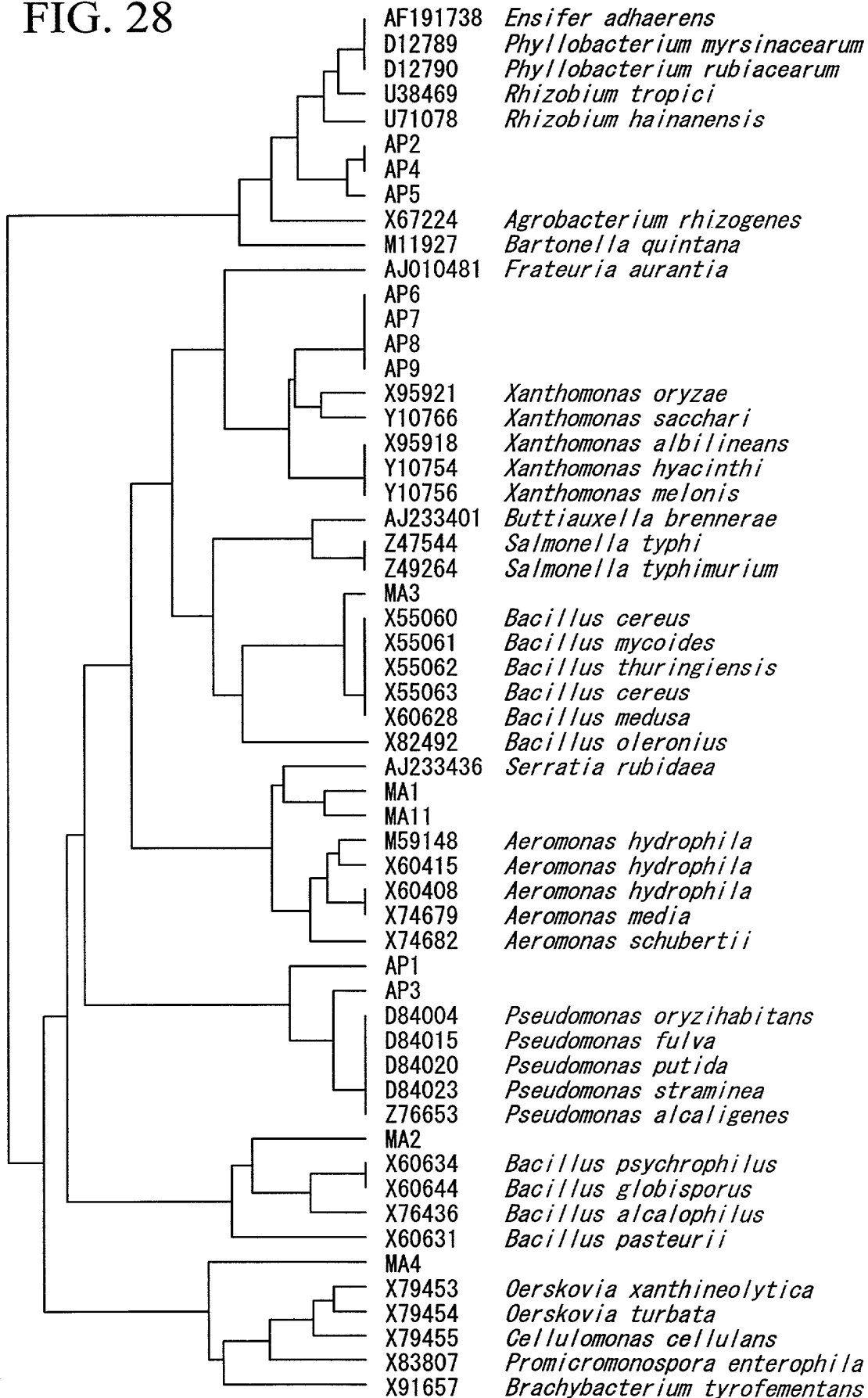


FIG. 28



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FIG. 29

CLASSIFICATION OF ISOLATED DENITRIFYING BACTERIA by 16S rDNA RFLP (RESTRICTION ENZYME
HaeIII, HhaI, AluI, RsaI, SrfI)
AND COMPARISON OF IDENTIFICATION RESULTS BY HOMOLGY SEARCH OF BASE SEQUENCES

GROUP	R OF BAC RFLP	BASE SEQUENCE (% HOMOLGY)
I	20	<i>Enterobacteriaceae</i>
II	9	<i>Burkholderia</i> genus.
III+IV	12	<i>Ralstonia</i> genus
V	6	<i>Comamonas acidovorans</i>
VI+VIII	32	<i>Pseudomonas</i> genus
VII	20	<i>P. putida</i>
IX	8	<i>P. rhodesiae</i>
X	5	<i>P. stutzeri</i>
XI	3	<i>Acinetobacter haemolyticus</i>
XII	18	<i>Pseudomonas</i> genus
XIII	1	<i>Acivorax delafieldii</i>